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OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:47 ; Search time 23 Seconds  
(without alignments)  
20.201 Million cell updates/sec

Title: US-09-756-899A-1  
Perfect score: 63  
Sequence: 1 AHWSGHCCL 9

Scoring table: BLOSUM62  
Gapop 13.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pep:\*  
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6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	55.6	8	2	US-08-557-122A-24
2	35	55.6	8	4	US-09-262-666-24
3	33	52.4	6	1	US-08-068-395A-4
4	33	52.4	6	1	US-08-464-365-4
5	33	52.4	6	3	US-08-627-907A-5
6	33	52.4	6	3	US-07-301-713A-1
7	33	52.4	7	2	US-08-323-536A-5
8	32	50.8	7	2	US-08-645-193B-65
9	28	44.4	8	3	US-08-657-339A-12
10	28	44.4	8	4	US-08-457-694A-12
11	26	41.3	4	1	US-07-609-716-10
12	26	41.3	4	1	US-08-477-509B-107
13	26	41.3	4	3	US-08-482-085B-107
14	26	41.3	4	3	US-08-475-411A-10
15	26	41.3	4	3	US-08-478-029A-10
16	26	41.3	4	4	US-09-444-791A-107
17	26	41.3	5	2	US-08-244-496-83
18	26	41.3	7	2	US-08-923-536A-6
19	26	41.3	9	3	US-09-258-754-368
20	26	41.3	9	3	US-09-042-107-368
21	26	41.3	9	4	US-09-722-2500-368
22	25	39.7	6	1	US-08-487-006-59
23	25	39.7	6	2	US-08-488-659A-59
24	25	39.7	6	4	US-09-058-740-6
25	25	39.7	8	2	US-08-520-535-12
26	25	39.7	8	2	US-09-079-432-12
27	25	39.7	9	3	US-09-518-046-63

Sequence 74, Appl  
Sequence 76, Appl  
Sequence 78, Appl  
Patent No. 5217955  
Sequence 4, Appl  
Sequence 5, Appl  
Sequence 3, Appl  
Sequence 17, Appl  
Sequence 20, Appl  
Sequence 17, Appl  
Sequence 3, Appl  
Sequence 17, Appl  
Sequence 20, Appl  
Sequence 27, Appl  
Sequence 8, Appl

US-09-270-542-74  
US-09-270-542-76  
US-09-270-542-78  
5217955-26  
US-07-733-095B-4  
US-07-826-328A-4  
US-07-826-328A-5  
US-07-973-235A-3  
US-08-350-884-17  
US-08-350-884-20  
US-08-709-173-17  
US-08-709-173-20  
US-08-482-720-3  
US-08-709-177-17  
US-08-709-177-20  
US-08-871-561-27  
US-09-321-932B-27  
US-07-836-928A-8

ALIGNMENTS

RESULT 1  
US-08-557-122A-24  
; Sequence 24: Application US/08557122A  
; Patent No. 5879664  
; GENERAL INFORMATION:  
; APPLICANT: Hjort, Carsten Mailand  
; TITLE OF INVENTION: Fungal Protein Disulfide Isomerase  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: No. 58796640 No. 5879664disk of No. 5879664th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/557,122A  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 3980.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-557-122A-24

Query Match 55.6%; Score 35; DB 2; Length 8;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AHWSGHC 7  
Db 1 AFWCGHC 7

RESULT 2

CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/068,395A  
FILING DATE: 19930527  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-195254  
FILING DATE: 27-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-44013  
FILING DATE: 04-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-44014  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Obolon, No. 5496719man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 68-228-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-3000  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-068-395A-4

Query Match 52.4%; Score 33; DB 1; Len  
Best Local Similarity 80.0%; Pred.No. 3e+05; 1;  
Matches 4; Conservative 0; Mismatches 1;

Qy 3 WSGHC 7  
| | | |  
Db 1 WCGHC 5

RESULT 4  
US-08-464-365-4  
Sequence 4, Application US/08464365  
Patent No. 5700659  
GENERAL INFORMATION:  
APPLICANT: YAMADA, YUKIO  
APPLICANT: ASAMI, OSAMU  
APPLICANT: SUGIYAMA, HIDEHIKO  
APPLICANT: IDEKOBA, CHIE  
APPLICANT: HOSHINO, FUMIHIKO  
APPLICANT: HIRAI, MASANA  
APPLICANT: KAJINO, TSUTOMU  
APPLICANT: INABA, TAKAO  
APPLICANT: SARAI, KIYOKO  
TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN  
TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING  
TITLE OF INVENTION: PRODUCING THE SAME  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & E  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,365  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-135254  
FILING DATE: 27-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-44013  
FILING DATE: 04-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-44014  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OSLON, NO. 5700859man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 68-228-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-464-365-4

Query Match 52.4%; Score 33; DB 1; Length 6;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WSGHC 7  
Db 1 WCGHC 5

RESULT 5  
US-08-627-907A-5  
Sequence 5, Application US/06627907A  
Patent No. 6060302  
GENERAL INFORMATION:  
APPLICANT: HIRANO, Naoto  
APPLICANT: HIRAI, Hisamaru  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA  
TITLE OF INVENTION: SEQUENCE ENCODING THE SAME  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSES: c/o FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,907A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-238402  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/01572  
FILING DATE: 22-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY Jr., James P.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-627-907A-5

Query Match 52.4%; Score 33; DB 3; Length 6;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WSGHC 7  
Db 1 WCGHC 5

RESULT 6  
US-07-901-713A-1  
Sequence 1, Application US/07901713A  
Patent No. 6291205  
GENERAL INFORMATION:  
APPLICANT: Tuite, Michael F.  
APPLICANT: Freedman, Robert B.  
APPLICANT: Markus, Henry Z.  
APPLICANT: Schultz, Loren D.  
APPLICANT: Montgomery, Donna L.  
APPLICANT: Ellis, Ronald W.  
TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF  
TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES  
TITLE OF INVENTION: CERREVISIAE  
FILE REFERENCE: 18469  
CURRENT APPLICATION NUMBER: US/07/901,713A  
CURRENT FILING DATE: 1992-06-12  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: vertebrate PDI active site  
US-07-901-713A-1

Query Match 52.4%; Score 33; DB 3; Length 6;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WSGHC 7  
Db 1 WCGHC 5

RESULT 7  
US-08-923-536A-5  
Sequence 5, Application US/08923536A  
Patent No. 5965426  
GENERAL INFORMATION:  
APPLICANT: SAKAI, Yasuyoshi  
APPLICANT: KATO, No. 5965426uo  
APPLICANT: SHIBANO, YUJI  
TITLE OF INVENTION: PROTEIN DISULFIDE ISOMERASE GENE DERIVED  
TITLE OF INVENTION: FROM STRAIN OF METHYLOTROPIC YEAST

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSES: BURNS, DONABE, SWECKER & MATHIS, L.L.P.  
STREET: 1737 King Street, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22314-2756  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/923,536A  
FILING DATE: 04-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-234287  
FILING DATE: 04-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meuth, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 001560-317  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-923-536A-5

Query Match 52.4%; Score 33; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MSGHC 7  
Db 2 WGHCC 6

RESULT 8  
US-08-645-193B-65  
Sequence 65, Application US/08645193B  
Patent No. 5962253  
GENERAL INFORMATION:  
APPLICANT: Kupke, Thomas  
APPLICANT: Gotz, Friedrich  
APPLICANT: Kempter, Christoph  
APPLICANT: Jung, Gunther  
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides  
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/645,193B  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.1540000  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-645-193B-65

Query Match 50.8%; Score 32; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MSGHCC 8  
Db 2 WNSYCC 7

RESULT 9  
US-08-657-339A-12  
Sequence 12, Application US/08657339A  
Patent No. 6265551  
GENERAL INFORMATION:  
APPLICANT: Duke-Cohan, Jonathan S.  
APPLICANT: Morimoto, Chikao  
APPLICANT: Schlossman, Stuart F.  
TITLE OF INVENTION: NOVEL FORM OF DIPEPTIDYLPEPTIDASE IV (CD26) FOUND IN  
TITLE OF INVENTION: HUMAN SERUM, ANTIBODIES THERETO, AND USES THEREFOR  
FILE REFERENCE: 00530-091001  
CURRENT APPLICATION NUMBER: US/08/657,339A  
CURRENT FILING DATE: 1996-06-03  
PRIOR APPLICATION NUMBER: US 08/457,694  
PRIOR FILING DATE: 1995-06-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-657-339A-12

Query Match 44.4%; Score 28; DB 3; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SGHCCL 9  
Db 1 SGHICI 6

RESULT 10  
US-08-457-694A-12  
Sequence 12, Application US/08457694A  
Patent No. 6325989  
GENERAL INFORMATION:  
APPLICANT: Duke-Cohan, Jonathan S.  
APPLICANT: Morimoto, Chikao  
APPLICANT: Schlossman, Stuart F.  
TITLE OF INVENTION: NOVEL FORM OF DIPEPTIDYLPEPTIDASE IV FOUND IN  
TITLE OF INVENTION: HUMAN SERUM  
FILE REFERENCE: 00530-090001  
CURRENT APPLICATION NUMBER: US/08/457,694A  
CURRENT FILING DATE: 1995-06-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 12

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;
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-457-694A-12

Query Match      44.4%; Score 28; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY      4 SGHCL 9
Db      1 SGHIC 6

RESULT 11
US-07-609-716-10
; Sequence 10, Application US/07609716
; Patent No. 5514581
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Functional Recombinantly Prepared
; TITLE OF INVENTION: Synthetic Protein Polymer
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/609,716
; FILING DATE: 06-NOV-1990
; CLASSIFICATION: 435
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-55186-3/BIR
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-609-716-10

Query Match      41.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HCC 8
Db      1 HCC 3

RESULT 12
US-08-477-509B-107
; Sequence 107, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W

; APPLICANT: Dorman, Mary A
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,518
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-509B-107

Query Match      41.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HCC 8
Db      1 HCC 3

RESULT 13
US-08-492-085B-107
; Sequence 107, Application US/08482085B
; Patent No. 6018030
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Pollock, Thomas J.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482.085B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,155  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-085B-107

Query Match 41.3%; Score 26; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HCC 8  
Db 1 HCC 3

RESULT 14  
US-08-475-411A-10  
Sequence 10, Application US/08475411A  
Patent No. 6140072  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Cappello, Joseph  
TITLE OF INVENTION: Functional Recombinantly Prepared  
TITLE OF INVENTION: Synthetic Protein Polymer  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,411A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/609,716  
FILING DATE: 06-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/269,429  
FILING DATE: 09-NOV-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/114,618  
FILING DATE: 29-OCT-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 04-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Trecartin, Richard F.  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-475-411A-10

Query Match 41.3%; Score 26; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HCC 8  
Db 1 HCC 3

RESULT 15  
US-08-478-029A-10  
Sequence 10, Application US/08478029A  
Patent No. 6184348  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A.  
APPLICANT: Cappello, Joseph  
TITLE OF INVENTION: Functional Recombinantly Prepared  
TITLE OF INVENTION: Synthetic Protein Polymer  
NUMBER OF SEQUENCES: 119  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,029A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/609,716  
FILING DATE: 06-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/269,429

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; FILING DATE: 09-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard P.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-8/RFT/MTX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-478-029A-10

Query Match 41.3%; Score 26; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HCC 8
Db 1 HCC 3

Search completed: June 1, 2004, 10:29:22
Job time : 24 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:46 ; Search time 21 Seconds  
(without alignments)  
41.225 Million cell updates/sec

Title: US-09-756-899A-1

Perfect score: 63

Sequence: 1 AHWGHCCCL 9

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.7	8	2 D61512	variant surface gl
2	23	36.5	9	2 A60522	sperm-activating p
3	21	33.3	8	2 C61512	variant surface gl
4	18	28.6	6	2 PT0652	T-cell receptor be
5	18	28.6	6	4 I79564	hypothetical TGL3
6	18	28.6	8	2 FC1002	leucine-tRNA ligas
7	18	28.6	9	2 QDRB	delta sleep-induci
8	18	28.6	9	2 A43848	cell surface adhes
9	18	28.6	9	2 PT0562	T-cell receptor be
10	18	28.6	9	2 PH0942	T-cell receptor be
11	17	27.0	4	2 B53284	T-cell receptor be
12	17	27.0	7	2 S08606	hypothetical prote
13	17	27.0	7	2 PT0642	T-cell receptor be
14	17	27.0	7	2 PT0728	T-cell receptor be
15	17	27.0	7	2 PT0786	T-cell receptor be
16	17	27.0	8	2 A25836	L-serine ammonia-1
17	17	27.0	9	2 A12872	transaldolase (EC
18	17	27.0	9	2 A11497	transaldolase (EC
19	17	27.0	9	2 PT0634	T-cell receptor be
20	16	25.4	5	2 PT0281	Ig heavy chain CRD
21	15.5	24.6	9	2 S07205	litorin 2-Glu - Au
22	15.5	24.6	9	2 S07204	litorin I - Austr
23	15.5	24.6	9	2 S07241	litorin - Rohde's
24	15	23.8	4	2 PT0661	T-cell receptor be
25	15	23.8	5	2 B45525	actin I - malaria
26	15	23.8	9	2 PT0231	Ig heavy chain CDR
27	15	23.8	9	2 A37027	macrophage chemota
28	14	22.2	3	3 GKHU	growth-modulating
29	14	22.2	4	2 PLO140	carbon-monoxide de

#### ALIGNMENTS

##### RESULT 1

D61512

variant surface glycoprotein MITat 1.6 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999

C;Accession: D61512

R;Holder: A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-term

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: D61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <HOL>

C;Keywords: glycoprotein

Query Match 39.7%; Score 25; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

3 WSGHCC 8

1 WEGETC 6

##### RESULT 2

A60522

sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)

C;Species: Diadema setosum

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000

C;Accession: A60522

R;Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzu

Comp. Biochem. Physiol. B 95, 423-429, 1990

A;Title: A species-specific sperm-activating peptide from the egg jelly of the sea urch

A;Reference number: A60522; MUID:90227916; PMID:2158412

A;Accession: A60522

A;Molecule type: protein

A;Residues: 1-9 <YOS>

C;Superfamily: unassigned animal peptides

F;2-9/Disulfide bonds: #status experimental

Query Match 36.5%; Score 23; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

3 WSGHCC 8

4 WGGAVC 9

##### RESULT 3

C61512

COI intron 16 prot  
sarcosine dehydrog  
collagen alpha 1(I)  
dermorphin (Trp-4,  
gramicidin S synth  
T-cell receptor be  
T-cell receptor be  
T-cell receptor ga  
sperm-activating p  
sperm-activating p  
probable minipolyp  
Ig heavy chain CRD  
D-amino-acid oxida  
biotin B - Citroba  
R-phycoerythrin ga  
R-phycoerythrin be

30 14 22.2 4 2 I38888  
31 14 22.2 6 2 A61419  
32 14 22.2 6 2 B56979  
33 14 22.2 7 2 S21230  
34 14 22.2 7 2 S24207  
35 14 22.2 7 2 PT0688  
36 14 22.2 8 2 PT0724  
37 14 22.2 8 2 A38887  
38 14 22.2 9 2 S19329  
39 14 22.2 9 2 JN0026  
40 14 22.2 9 2 B45020  
41 14 22.2 9 2 PT0324  
42 14 22.2 9 2 S39437  
43 13 20.6 5 2 I40698  
44 13 20.6 5 2 P22565  
45 13 20.6 6 2 C22565



```

A;Reference number: 159162; MOLID:50222105; EMBL:U02202.1.
A;Accession: 179564
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-6 <ZUT>
A;Cross-references: GB:M33602; NID:G339907; PIDN:AAA66449.1; PID:G807656
C;Comment: This is the hypothetical translation of a sequence translated in an incorrect
Query Match      28.6%; Score 18; DB 4; Length 6;
Best Local Similarity 100.0%; Prod. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CC 8
        ||
        ||
Db      3 CC 4

```

C>Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
C:Accession: A43848  
R:Jiang, O.D.; Ascencio, F.; Evanson, L.A.; Wadstrom, T.  
Infect. Immun. 60: 899-906, 1992  
A:Title: Binding of heparan sulfate to *Staphylococcus aureus*.  
A:Reference number: A43848; MUID:92176005; PMID:1541563  
A:Accession: A43848  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <11A>  
A:Note: sequence extracted from NCBI backbone (NCBIP:85442)  
  
Query Match 28.6%; Score 18; DB 2: Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;



A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0586  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <PEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-iCN and 141-ICD)  
C;Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. NO. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSG 5  
| |  
Db 5 WGG 7

RESULT 15

PT0728  
T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0728  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0728  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <PEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. NO. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WSG 5  
| |  
Db 5 WGG 7

Search completed: June 1, 2004, 10:28:46  
Job time : 22 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:45 ; Search time 11 Seconds  
(without alignments)  
42.603 Million cell updates/sec

Title: US-09-756-899A-1

Perfect score: 63

Sequence: 1 AHWGHCCL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	28.6	9	1 DSIP_RABIT	P01158
2	17	27.0	9	1 TALL_PICUA	P17440
3	17	27.0	9	1 TALL_PICUA	P17441
4	16	25.4	9	1 COW_CONVE	P83047
5	15.5	24.6	9	1 LIT0_LITAU	P08945
6	15.5	24.6	9	1 LITR_PHYRO	P08946
7	15	23.8	5	1 UF01_MOUSE	P38639
8	15	23.8	9	1 NEP_HV128	P12481
9	14	22.2	3	1 GRWY_HUMAN	P01157
10	14	22.2	4	1 DCM1_PSECH	P19916
11	14	22.2	9	1 MOSH_CLYJA	P19852
12	14	22.2	9	1 NSK1_SARBU	P41492
13	14	22.2	9	1 SAP_STOVA	P24047
14	13	20.6	5	1 BIO1_CITFR	P12997
15	13	20.6	9	1 DNFI_LOCFI	P16339
16	13	20.6	9	1 LMIP_LOCFI	P31799
17	13	20.6	9	1 PKK1_PPRAM	P82691
18	12	19.0	5	1 BPP7_BOTIN	P30425
19	12	19.0	6	1 TRP1_PSEPU	P36414
20	12	19.0	8	1 COW2_CONFU	P58785
21	12	19.0	8	1 HTF1_PPRAM	P04548
22	12	19.0	8	1 HTF2_PPRAM	P04549
23	12	19.0	8	1 HTP_TENNO	P25419
24	12	19.0	8	1 XYL4_STRSQ	P19149
25	11	17.5	4	1 OCP3_OCTMI	P58649
26	11	17.5	6	1 E101_LITRU	P82096
27	11	17.5	6	1 LOK1_LOCFI	P41491
28	11	17.5	7	1 BRHP_CONIM	P58803
29	11	17.5	7	1 TPFY_PACDA	P83455
30	11	17.5	7	1 TY51_LITRU	P82065
31	11	17.5	7	1 WWA1_ACHFU	P35919
32	11	17.5	7	1 WWA2_ACHFU	P35920
33	11	17.5	7	1 WWA3_ACHFU	P35921

```

34 11 17.5 8 1 AC1_THUAL P18691 thunnus alb
35 11 17.5 8 1 AKHG_GRYBI P14086 gryllus bim
36 11 17.5 8 1 AKH_LIBAU P25418 libellula a
37 11 17.5 8 1 AKH_MELML P25423 melolontha
38 11 17.5 8 1 AKH_TABAT P14595 tabanus atr
39 11 17.5 8 1 ALLI_CYDPO P82152 cydia pomon
40 11 17.5 8 1 CCKN_MACEU P30369 macropus eu
41 11 17.5 8 1 LCK1_LEUMA P21140 leucophaea
42 11 17.5 8 1 LCK2_LEUMA P21141 leucophaea
43 11 17.5 8 1 LCK3_LEUMA P21142 leucophaea
44 11 17.5 8 1 LCK4_LEUMA P21143 leucophaea
45 11 17.5 8 1 LCK5_LEUMA P19987 leucophaea

```

#### ALIGNMENTS

```

RESULT 1
DSIP_RABIT
ID_DSIP_RABIT STANDARD; PRT; 9 AA.
AC P01158;
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Delta sleep-inducing peptide (DSIP).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=77185324; PubMed=862769;
RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA Schoenenberger G.A.;
RT "The delta sleep inducing peptide (DSIP). Comparative properties of
RT the original and synthetic nonapeptide.";
RL Experimentia 33:548-552(1977).
RN [2]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=79054421; PubMed=568769;
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
RT analysis, sequence, synthesis and activity of the nonapeptide.";
RN [3]
RP FLUGERS ARCH. 376:119-129(1978).
RX REVIEW.
RX MEDLINE=87175129; PubMed=3550726;
RA Graf M.V., Kaetin A.J.;
RT "Delta-sleep-inducing peptide (DSIP): an update.";
RL Peptides 7:1165-1187(1986).
CC -!- FUNCTION: When infused into the mesodiencephalic ventricle of
CC recipient rabbits induces spindle and delta EEG activity and
CC reduced motor activities.
CC -!- MISCELLANEOUS: This peptide was obtained from dialysates of
CC occipital venous sinus blood from rabbits kept asleep by electric
CC stimulation of the thalamus.
CC -!- DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 8 of March 2001;
CC WWW="http://www.expasy.org/spotlight/articles/split008.html".
DR PIR: A01422; QDRB.
SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;

```

Query Match 28.6%; Score 18; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSG 5  
| |  
D0 1 WAG 3

RESULT 2  
TALL\_PICUA

FT NON TER 9 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 27.0%; Score 17; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HC 7  
DB 4 HC 5

RESULT 4  
COW\_CONVE STANDARD; PRT; 9 AA.

ID \_COW CONVE STANDARD; PRT; 9 AA.  
AC P83047;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Contryphan-Vn.  
OS Conus ventricosus (Mediterranean cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsgastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
NCBI\_TaxID=117992;  
[1]  
RN SEQUENCE, SYNTHESIS, DISULFIDE BONDS, AND MASS SPECTROMETRY.  
RP TISSUE=Venom;  
RC MEDLINE=21547785; PubMed=11688995;  
RX Massilia G.R., Schinina M.E.; Ascenzi P., Politicelli F.;  
RA "Contryphan-Vn: a novel peptide from the venom of the Mediterranean  
snail Conus ventricosus.";  
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).  
[2]  
RN STRUCTURE BY NMR, SYNTHESIS, DISULFIDE BONDS, AND FUNCTION.  
RP MEDLINE=22533239; PubMed=12646193;  
RX Massilia G.R., Eliseo J., Grolleau F., Lapied B., Barbier J.,  
RA Bournaud R., Molgo J., Cicero D.O., Paci M., Schinina M.E.,  
RA Ascenzi P., Politicelli F.;  
RP "Contryphan-Vn: a modulator of Ca2+-dependent K+ channels.";  
RL Biochem. Biophys. Res. Commun. 303:238-246(2003).  
CC -I- FUNCTION: Affects both voltage-gated and calcium-dependent  
potassium channel activities, with composite and diversified  
effects in invertebrate and vertebrate systems.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -I- PTM: The cis isomer is the most abundant and is thus thought to be  
the functionally relevant conformer.  
CC -I- MASS SPECTROMETRY: MW=1088.6; METHOD=NALDI.  
CC -I- SIMILARITY: Belongs to the contryphan family.  
DR PB; LNXN; 04-MAR-03  
KW Toxin; Ionic channel inhibitor; Neurotoxin;  
KW Potassium channel inhibitor; D-amino acid; Amidation; 3D-structure.  
LITO LITAU STANDARD; PRT; 9 AA.  
ID \_LITO LITAU STANDARD; PRT; 9 AA.  
AC P8945;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)

QY 3 WSGHC 7  
DB 5 WKPC 9

Query Match 25.4%; Score 16; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WSGHC 7  
DB 5 WKPC 9

RESULT 5  
LITO LITAU STANDARD; PRT; 9 AA.  
ID \_LITO LITAU STANDARD; PRT; 9 AA.  
AC P8945;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Litorin.  
 OS Litoria aurea (Green and golden bell frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=8371;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=75187011; PubMed=1140241;  
 RA Anastasi A., Erspamer V., Endean R.;  
 RT "Amino acid composition and sequence of litorin, a bombesin-like  
 nonapeptide from the skin of the Australian leptodactylid frog  
 Litoria aurea.";  
 RL Experientia 31:510-511 (1975).  
 RN [2]  
 RP SEQUENCE, AND METHYLATION OF GLN-2.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=78003546; PubMed=908397;  
 RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;  
 RT "Glu(Ome)3-litorin, the second bombesin-like peptide occurring in  
 methanol extracts of the skin of the Australian frog Litoria aurea.";  
 RL Experientia 33:1289-1289 (1977).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin  
 family.  
 DR PIR: S07204; S07204.  
 DR PIR: S07205; S07205.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 DR Amphibian defense peptide; Bombesin family; Amidation;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 2 2 DEAMIDATION AND METHYLATION (PARTIAL).  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1103 MW; D7CCC1E862CDC366 CRC64;  
 Query Match 24.6%; Score 15.5; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 QY 3 WS-GH 6  
 DB 3 WAVGH 7

RESULT 6  
 ID\_LITE\_PHYTO STANDARD; PRT; 9 AA.  
 AC P08946;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rhodiola-litorin.  
 OS Phylomedusa rohdei (Rohde's leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 OX NCBI\_TaxID=8394;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=85127560; PubMed=3838283;  
 RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,  
 RA Erspamer V.;  
 RT "Rhodiola-litorin: a new peptide from the skin of Phyllomedusa rohdei.";  
 RL FEBS Lett. 182:53-56 (1985).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin

family.  
 DR PIR: S07241; S07241.  
 DR InterPro: IPR000874; Bombesin.  
 DR Pfam: PF02044; Bombesin; 1.  
 DR PROSITE: PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1090 MW; 4ECCC1E861ADC377 CRC64;  
 Query Match 24.6%; Score 15.5; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
 QY 3 W-SGH 6  
 DB 3 WAVGH 7

RESULT 7  
 ID\_UF01\_MOUSE STANDARD; PRT; 5 AA.  
 AC P38639;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (F19) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=9500907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745 (1994).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 protein is: 6.6, its MW is: 19 kDa.  
 FT NON\_TER 5  
 SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;  
 Query Match 23.8%; Score 15; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 WSG 5  
 DB 1 WIG 3

RESULT 8  
 ID\_NEF\_HV128 STANDARD; PRT; 9 AA.  
 AC P12481;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Negative factor (P-protein) (27 kDa protein) (3'ORF) (Fragment).  
 GN NEF.  
 OS Human immunodeficiency virus type 1 (2-84 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retrovirus.  
 OX NCBI\_TaxID=11681;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88281279; PubMed=3395517;  
 RA Younso J., Josephs S.P., Reitz M.S. Jr., Zagury D., Wong-Staal F.,  
 RA Gallo R.C.;  
 RT "Nucleotide sequence analysis of the env gene of a new Zairian  
 isolate of HIV-1.";

END OF REPORT

**ध्यातः नावोत्तः त् धर्म्मो नृ/ एव सन्**

**March 1, 2017**

**March 1, 2017**

**ध्यातः नावोत्तः त् धर्म्मो नृ/ एव सन्**

**ध्यातः नावोत्तः त् धर्म्मो नृत्तः एव सन्**

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNC 7  
DB 6 GNC 8

RESULT 12  
NSKL\_SARBU STANDARD; PRT; 9 AA.  
AC P41452;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Neosulfakinin-I (NEB-SK-I).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RX MEDLINE=93083101; PubMed=1360367;  
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
RT "Isolation and primary structure of two sulfakinin-like peptides from  
the fleshfly, Neobellieria bullata.";  
RL Comp. Biochem. Physiol. 103C:135-142(1992).  
CC -|- SIMILARITY: Myotropic peptide.  
CC -|- FUNCTION: Belongs to the gastrin/cholecystokinin family.  
DR InterPro: IPR001651; Gastrin.  
DR PROSITE: PS00259; GASTRIN; 1.  
KW Neuropeptide; Amidation; Sulfation.  
FT MOD RES 4 4 SULFATION (POTENTIAL).  
FT MOD RES 9 9 AMIDATION (POTENTIAL).  
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;

Query Match 22.2%; Score 14; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GH 6  
DB 5 GH 6

RESULT 13  
SAP\_STOVA STANDARD; PRT; 9 AA.  
AC P24047;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Sperm-activating peptide (SAP).  
OS Stomopneustes variolaris (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;  
OC Stomopneustes.  
OX NCBI\_TaxID=7663;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BOND.  
RC TISSUE=Egg jelly;  
RX MEDLINE=92097763; PubMed=1756858;  
RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;  
RT "Determination of the amino acid sequence of an intramolecular  
disulfide linkage-containing sperm-activating peptide by tandem mass  
spectrometry.";  
RL FEBS Lett. 294:179-182(1991).  
CC -|- FUNCTION: Cause stimulation of sperm respiration and motility  
through intracellular alkalinization, transient elevations of  
cAMP, cGMP and calcium levels in sperm cells, and transient  
activation and subsequent inactivation of the membrane form of  
guanylate cyclase.  
FT DISULFID 3 8  
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match 22.2%; Score 14; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;

QY 5 GH 6  
DB 5 GH 6

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNC 7  
DB 6 GNC 8

RESULT 14  
BIOB\_CITER STANDARD; PRT; 5 AA.  
AC P12997;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).  
GN BIOB.  
OS Citrobacter freundii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Citrobacter.  
OX NCBI\_TaxID=546;  
RN [1]  
RP SEQUENCE FROM N.A. PubMed=2971595;  
RX MEDLINE=89006280; PubMed=2971595;  
RA Shiuan D., Campbell A.;  
RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
Citrobacter freundii and Salmonella typhimurium biotin operons.";  
RL Gene 67:203-211(1988).  
CC -|- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.  
CC -|- PATHWAY: Biotin biosynthesis; last step.  
CC -|- SIMILARITY: Belongs to the biotin and lipoic acid synthetases  
family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M21922; -; NOT\_ANNOTATED\_CDS.  
DR EIR; 140698; 140698.  
KW Biotin biosynthesis; Iron-sulfur; Transferase.  
FT NON\_TER 5 5  
SQ SEQUENCE 5 AA; 532 MW; 75A5B1BDD6F00000 CRC64;

Query Match 20.6%; Score 13; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AHS 4  
DB 2 AHS 5

RESULT 15  
DNFL\_LOCHI STANDARD; PRT; 9 AA.  
AC P16339;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Locupressin (Diuretic neuropeptide F1/F2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Subesophageal ganglion, and Thoracic ganglion;  
RX MEDLINE=88077077; PubMed=3689410;  
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,

Query Match 22.2%; Score 14; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;

QY 5 GH 6  
DB 5 GH 6



RA Delaage M., Schooley D.A.;  
RT "Identification of an arginine vasopressin-like diuretic hormone from  
RL Locusta migratoria";  
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).  
CC -!- FUNCTION: DIURETIC HORMONE.  
CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.  
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.  
DR PIR; A29477; A29477.  
DR InterPro; IPR000981; Neurhvp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Neuropeptide; Amidation.  
FT DISULFID 1 6 IN F1.  
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).  
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).  
FT MOD RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;  
  
Query Match 20.6%; Score 13; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 CL 9  
Db 1 CL 2  
  
Search completed: June 1, 2004, 10:27:20  
Job time : 13 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:46 ; Search time 39 Seconds  
(without alignments)  
72.812 Million cell updates/sec

Title: US-09-756-899A-1  
Perfect score: 63  
Sequence: 1 AHWGHCCL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_todent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	34.9	9	10 Q9FSZ2	Q9FSZ2 cicer ariet
2	19.5	31.0	8	6 O02831	O02831 oryctolagus
3	19	30.2	8	4 Q8IV87	Q8IV87 homo sapien
4	19	30.2	9	8 Q8W8X4	Q8W8X4 diadema mex
5	18	28.6	8	13 Q98TU5	Q98TU5 xenopus lae
6	18	28.6	9	2 Q9S5M1	Q9S5M1 staphylococ
7	18	28.6	9	11 Q08979	Q08979 mus musculu
8	18	28.6	9	12 Q9E1U7	Q9E1U7 hepatitis b
9	17	27.0	8	4 Q15900	Q15900 homo sapien
10	17	27.0	9	4 Q99887	Q99887 homo sapien
11	17	27.0	9	15 Q85723	Q85723 simian sarc
12	16	25.4	9	8 Q94NB1	Q94NB1 microcebus
13	16	25.4	9	8 Q94NB2	Q94NB2 microcebus
14	16	25.4	9	8 Q94NA9	Q94NA9 daubentonia
15	16	25.4	9	8 Q94XE6	Q94XE6 tectocoris
16	16	25.4	9	8 Q94NB0	Q94NB0 microcebus

17	16	25.4	9	8 Q85DB8	Q85DB8 lepilemur e
18	16	25.4	9	8 Q85DB0	Q85DB0 lepilemur s
19	15	23.8	8	4 Q15888	Q15888 homo sapien
20	15	23.8	8	8 Q94VC1	Q94VC1 varanus rud
21	15	23.8	8	8 Q9TD02	Q9TD02 terranatos
22	15	23.8	8	8 Q94PX5	Q94PX5 felis silve
23	15	23.8	8	8 Q94VB2	Q94VB2 varanus sal
24	15	23.8	8	8 Q94PX7	Q94PX7 felis silve
25	15	23.8	8	8 Q94PX6	Q94PX6 felis libyc
26	15	23.8	8	8 Q94VA7	Q94VA7 varanus sal
27	15	23.8	8	8 Q94VB5	Q94VB5 varanus sal
28	15	23.8	8	11 P82598	P82598 rattus norv
29	15	23.8	8	12 Q64971	Q64971 alfalfa mos
30	15	23.8	9	2 Q47410	Q47410 escherichia
31	15	23.8	9	4 Q9UC36	Q9UC36 homo sapien
32	15	23.8	9	8 Q94VH4	Q94VH4 varanus gla
33	15	23.8	9	8 Q94VH8	Q94VH8 varanus ere
34	15	23.8	9	8 Q94VC6	Q94VC6 varanus pil
35	15	23.8	9	13 Q9PRJ4	Q9PRJ4 lepisosteus
36	14	22.2	7	10 P82445	P82445 nicotiana t
37	14	22.2	8	6 Q9TRV3	Q9TRV3 sus sp. ins
38	14	22.2	9	4 Q15999	Q15999 homo sapien
39	14	22.2	9	12 Q89491	Q89491 murine minu
40	13	20.6	7	12 Q66113	Q66113 cherry leaf
41	13	20.6	7	13 Q42564	Q42564 fugu rubrip
42	13	20.6	8	2 Q85406	Q85406 coxiella bu
43	13	20.6	9	2 Q47063	Q47063 escherichia
44	13	20.6	9	4 Q9UMF3	Q9UMF3 homo sapien
45	13	20.6	9	11 Q61723	Q61723 mus musculu

#### ALIGNMENTS

##### RESULT 1

Q9FSZ2 PRELIMINARY; PRT; 9 AA.  
AC Q9FSZ2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DB Hypothetical protein (Fragment).  
OS Cicer arietinum (Chickpea) (Garbanzo).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.  
CX NCBI\_TaxID=3827;  
[1]  
RN SEQUENCE FROM N.A.  
RP SFRAIN-cv. Castellana; TISSUE=Etiolated epicotyl;  
RC Dopico B., Jimenez T., Labrador E.;  
RA "cDNA clones expressed in etiolated Cicer arietinum epicotyls.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ299069; CAC10216.1; -  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 9 AA; 990 MW; 9441BDDAA7272EBB CRC64;

Query Match 34.9%; Score 22; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 16+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCL 9  
Db 2 CCL 4

##### RESULT 2

O02831 PRELIMINARY; PRT; 8 AA.  
ID O02831  
AC O02831;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Pro alpha 1 type III collagen protein (fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96377332; PubMed=8781186;  
 RA Metsarantha M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
 RA Vuorio E.;  
 RT "Evidence for insufficient chondrocytic differentiation during repair  
 RT of full-thickness defects of articular cartilage.";  
 RL Matrix Biol. 15:39-47(1996).  
 DR EMBL; S83371; AAD14433.1; -.  
 RN Collagen.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA7371 CRC64;  
 QY  
 Db  
 RESULT 3  
 Q8IV87 PRELIMINARY; PRT; 8 AA.  
 AC Q8IV87  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit  
 DE 2-like (Aminotransferase 2), variant 1) (Fragment).  
 GN SPILC21.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith M.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL050320; CAD54807.1; -.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Transferase.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 908 MW; 8E533682CEB8B042 CRC64;  
 QY  
 Db  
 Query Match 30.2%; Score 19; DB 4; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CCL 9  
 Db 3 CCV 5  
 RESULT 4  
 Q8W8X4 PRELIMINARY; PRT; 9 AA.  
 AC Q8W8X4  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit II (fragment).  
 GN COII.  
 OS Diadema mexicanum.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;  
 OC Diadema.  
 OX NCBI\_TaxID=105359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CC70, and CC117;  
 RX MEDLINE=21323357; PubMed=11430656;  
 RA Lessios H.A., Kessing B.D., Pearse J.S.;  
 RT "Population structure and speciation in tropical seas: global  
 RT phylogeography of the sea urchin *Diadema*.";  
 RL Evolution 55:955-975(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CC70, and CC117;  
 RX MEDLINE=21561594; PubMed=11703875;  
 RA Lessios H.A., Garrido M.J., Kessing B.D.;  
 RT "Demographic history of *Diadema antillarum*, a keystone herbivore on  
 RT Caribbean reefs.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).  
 DR EMBL; AY012920; AAL3843.1; -.  
 DR EMBL; AY012921; AAL3844.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 1174 MW; 2B73173B46DDC2D3 CRC64;  
 QY 2 HW 3  
 Db 1 HW 2  
 RESULT 5  
 Q98TU5 PRELIMINARY; PRT; 8 AA.  
 AC Q98TU5  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ElrD transcript 2 (fragment).  
 GN ELRD.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21226152; PubMed=11327714;  
 RA Nassar F., Wegnez M.;  
 RT "Characterization of two promoters of the *Xenopus laevis* elrD gene.";  
 RL Biochem. Biophys. Res. Commun. 283:392-398(2001).  
 DR EMBL; AF329448; AAK01428.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 1008 MW; FF93372874537B16 CRC64;  
 QY 3 WSG 5  
 Db 3 WNG 5  
 RESULT 6  
 Q9R5M1 PRELIMINARY; PRT; 9 AA.  
 AC Q9R5M1  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE.
RX MEDLINE=92176005; PubMed=1541563;
RA Ljung O.D., Ascencio F., Fransson L.A., Wadstrom T.;
RT "Binding of heparan sulfate to Staphylococcus aureus.";
RL Infect. Immun. 60:899-906(1992).
DR PIR; A43848; A43848.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 990 MW; 2289DD7337861B3 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSG 5
DB 2 WTG 4

RESULT 7
Q08979 ID C08979 PRELIMINARY; PRT; 9 AA.
AC C08979;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE AML1 protein (fragment).
DE AML1.
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen P.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776DB CRC64;

Query Match 28.6%; Score 18; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGH 6
DB 5 SGH 7

RESULT 8
Q9E1U7 ID Q9E1U7 PRELIMINARY; PRT; 9 AA.
AC Q9E1U7;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE X protein (fragment).
DE X.
GN X.
OS Hepatitis B virus.
OC Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21213459; PubMed=11315638;
RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Kim Y.;
RT "Sequence variation of Hepatitis B virus promoter regions in
RT persistently infected patients.";
RL Arch. Virol. 146:279-292(2001).
DR EMBL; AF276526; AAG29993.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 994 MW; CD0FDEBEA2D40DD CRC64;

Query Match 28.6%; Score 18; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CC 8
DB 6 CC 7

RESULT 9
Q15900 ID Q15900 PRELIMINARY; PRT; 8 AA.
AC Q15900;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE (Clone XP7B11A) (Fragment).
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yardeni A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32079; AAA73890.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 27.0%; Score 17; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HC 7
DB 1 HC 2

RESULT 10
Q99887 ID Q99887 PRELIMINARY; PRT; 9 AA.
AC Q99887;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE 11 <beta>-HSD2 protein (fragment).
DE 11 <BETA>-HSD2.
GN 11 <BETA>-HSD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96133030; PubMed=8538347;
```

RA Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,  
 RA Sheppard M.C., Whorwood C.B.;  
 RT "Hypertension in the syndrome of apparent mineralocorticoid excess due  
 to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene.";  
 RL Lancet 347:88-91(1996).  
 DR EMBL; S80133; RAD14324.1; -  
 DR GO; GO:0003845; F11-beta-hydroxysteroid dehydrogenase activity; NAS.  
 DR GO; GO:0008212; P:iminoalcoholcorticoid metabolism; NAS.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1020 MW; C3FC2BB1F5B059C9 CRC64;  
 Query Match 27.0%; Score 17; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;  
 Qy 6 HC 7  
 Db 6 HC 7

RESULT 11  
 Q85723  
 ID Q85723 PRELIMINARY; PRT; 9 AA.  
 AC Q85723;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE V-sis and p28-sis genes (Fragment).  
 OS Simian sarcoma virus.  
 OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.  
 OC NCBI\_TaxID=11817;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84106822; PubMed=6319011;  
 RA Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;  
 RT "Expression of the PDGF-related transforming protein of simian sarcoma  
 virus in E. coli.";  
 RL Cell 36:43-49(1984).  
 DR EMBL; X01473; AAA46816.1; -  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;  
 Query Match 27.0%; Score 17; DB 15; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1e+06; Indels 1; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 1;  
 Qy 3 MSG 5  
 Db 5 MQG 7

RESULT 12  
 Q94NB1  
 ID Q94NB1 PRELIMINARY; PRT; 9 AA.  
 AC Q94NB1;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN COIII.  
 OS Microcebus ravelobensis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
 OC Microcebus.  
 OC NCBI\_TaxID=122231;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=JP299, and JP301;  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)  
 based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 DR EMBL; AF224630; AAK70571.1; -  
 DR EMBL; AF224631; AAK70575.1; -  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 25.4%; Score 16; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06; Indels 1; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 1;  
 Qy 2 HMSG 5  
 Db 5 YWVG 8

RESULT 13  
 Q94NB2  
 ID Q94NB2 PRELIMINARY; PRT; 9 AA.  
 AC Q94NB2;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN COIII.  
 OS Microcebus murinus (Lesser mouse lemur).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
 OC Microcebus.  
 OC NCBI\_TaxID=30608;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=JP285, JP288, JP289, JP292, JP308, and JP313;  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates)  
 based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 DR EMBL; AF224624; AAK70547.1; -  
 DR EMBL; AF224625; AAK70551.1; -  
 DR EMBL; AF224626; AAK70555.1; -  
 DR EMBL; AF224627; AAK70559.1; -  
 DR EMBL; AF224628; AAK70563.1; -  
 DR EMBL; AF224629; AAK70567.1; -  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 25.4%; Score 16; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1e+06; Indels 1; Gaps 0;  
 Matches 2; Conservative 1; Mismatches 1;  
 Qy 2 HMSG 5  
 Db 5 YWVG 8

RESULT 14  
 Q94NA9  
 ID Q94NA9 PRELIMINARY; PRT; 9 AA.  
 AC Q94NA9;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN COIII.  
 OS Daubentonia madagascariensis (Aye-aye).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;

OC Daubentonina.  
OX NCBI\_TaxID=31869;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=JP119, and JP120;  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family Cheirogaleidae (Primates)  
RT based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
DR EMBL: AF224641; AAK70615.1; -  
DR EMBL: AF224642; AAK70619.1; -  
DR GO: 0005739; C:mitochondrion; IEA.  
XW Mitochondrion.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 25.4%; Score 16; DB 8; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HWSG 5  
Db 5 YWNG 8

RESULT 15

Q94XE6 PRELIMINARY; PRT; 9 AA.  
AC Q94XE6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit III (Fragment).  
GN COX3.  
OS Tectocoris diopthalmus (cotton harlequin bug).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
OC Pentheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
OC Tectocoris.  
OX NCBI\_TaxID=159956;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP MEDLINE=21396409; PubMed=11504862;  
RA Shao R., Campbell N.J.H., Schmidt E.R., Barker S.C.;  
RT "Increased rate of gene rearrangement in the mitochondrial genomes of  
RT three orders of hemipteroid insects.";  
RL Mol. Biol. Evol. 18:1828-1832(2001).  
DR EMBL: AF335990; AAK55283.1; -  
DR GO: 0005739; C:mitochondrion; IEA.  
XW Mitochondrion.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;

Query Match 25.4%; Score 16; DB 8; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HWSG 5  
Db 5 YWNG 8

Search completed: June 1, 2004, 10:28:14  
Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 1, 2004, 10:25:45 ; Search time 54 Seconds  
(without alignments)  
47.091 Million cell updates/sec

Title: US-09-756-899A-1

Perfect score: 63

Sequence: 1 AARSHGCLL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	9	3 AAV77664	AAV77664 Immunoglobulin
2	63	100.0	9	7 AAV77664	AAV77664 Immunoglobulin
3	36	57.1	8	2 AAY21052	AAY21052 Human Gli
4	35	55.6	8	4 AAB49950	AAB49950 Protein d
5	35	55.6	9	4 AAB49952	AAB49952 Protein d
6	33	52.4	6	4 AAB49951	AAB49951 Protein d
7	33	52.4	6	5 ABP54937	ABP54937 Active si
8	33	52.4	7	2 AAW56315	AAW56315 Active ce
9	32	50.8	7	2 AAY43470	AAY43470 Flavoprot
10	32	50.8	9	5 AAE19859	AAE19859 TRIP zinc
11	31	49.2	9	4 AAM23018	AAM23018 HIV Pepti
12	31	49.2	9	4 AAM23018	AAM23018 HIV Pepti
13	31	49.2	9	4 AAM23018	AAM23018 HIV Pepti
14	30	47.6	9	4 AAU24423	AAU24423 Human MHC
15	30	47.6	9	4 AAU24423	AAU24423 Human MHC
16	29	46.0	9	5 ABB05276	ABB05276 Vascular
17	29	46.0	9	2 AAW6789	AAW6789 Lamprey I
18	29	46.0	9	2 AAW6789	AAW6789 Lamprey I
19	28	44.4	8	4 AAB50022	AAB50022 Mutant an
20	28	44.4	9	2 AAB85445	AAB85445 Chymotryp
21	28	44.4	9	2 AAR89336	AAR89336 Luteinisi
22	28	44.4	9	4 AAW43842	AAW43842 Specific
23	28	44.4	9	4 AAM22404	AAM22404 HIV pepti
24	28	44.4	9	4 AAM23297	AAM23297 HIV pepti
25	28	44.4	9	4 AAM23021	AAM23021 HIV pepti
					AAM23295 HIV pepti

26	28	44.4	9	6 ABR75265	ABR75265 Biologica
27	28	44.4	9	7 ABR56215	ABR56215 Luteinisi
28	27.5	43.7	9	7 ADD70027	ADD70027 Bombesin/
29	27	42.9	8	1 AAP71501	AAP71501 Growth ho
30	27	42.9	8	2 AAR73339	AAR73339 Human TSH
31	27	42.9	8	2 AAR73340	AAR73340 Human TSH
32	27	42.9	8	2 AAW30454	AAW30454 Somatosta
33	27	42.9	9	1 AAP71502	AAP71502 Growth ho
34	27	42.9	9	1 AAP82065	AAP82065 Polypepti
35	27	42.9	9	2 AAR43763	AAR43763 MHC Class
36	27	42.9	9	2 AAW39681	AAW39681 HPV16 E6
37	27	42.9	9	2 AAW30461	AAW30461 Somatosta
38	27	42.9	9	2 AAW54748	AAW54748 Peptide f
39	27	42.9	9	4 AAU02357	AAU02357 HLA bindi
40	27	42.9	9	5 ABJ04593	ABJ04593 Bone marr
41	27	42.9	9	6 ABJ60234	ABJ60234 184P182-r
42	26	41.3	4	3 AAY78293	AAY78293 Metalloth
43	26	41.3	4	4 AAB63980	AAB63980 Metal bin
44	26	41.3	4	4 AAB72710	AAB72710 Repetitiv
45	26	41.3	4	5 ABG69284	ABG69284 Metalloth

#### ALIGNMENTS

#### RESULT 1

AAV77664

ID AAV77664 standard; peptide; 9 AA.

XX AAV77664;

DT 12-MAY-2000 (first entry)

DE Immunoglobulin (Ig) free light chain binding peptide LCBP.

XX Immunoglobulin; Ig; light chain; LC; multiple sclerosis; antiasthmatic;  
XX antiallergy; chronic inflammatory bowel disorder; antiinflammatory;  
XX antiviral; virucide; neuroprotective; antimigraine.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetylation"

FT Modified-site 9 /note= "C-terminal amide"

FT WO200002915-A1.

XX 20-JAN-2000.

XX 07-JUL-1999; 99WO-NL000430.

XX 09-JUL-1998; 98NL-01009601.

XX (UUT-) RIJXSUNIV UTRECHT.

XX Redegeld FAM, Kraneveld AD, Nijkamp FP;

XX WPI; 2000-171132/15.

XX New compounds which inhibit immunoglobulin light chain binding to mast cells, used for treating, e.g. asthma.

PS Claim 2; Page 13; 26pp; English.

XX The invention relates to compounds which inhibit the binding of the free light chain (LC) of immunoglobulin (Ig) to mast cells. The compounds can be used for treating e.g. asthma, allergy, chronic inflammatory bowel disorders, viral infection or multiple sclerosis, and possibly migraine. The methods can also be used for diagnosing a disease in a patient having an elevated level of the free LC of Ig in a body fluid. The present sequence represents a peptide capable of binding to the free LC of Ig

XX Sequence 9 AA;  
SQ

Query Match 100.0%; Score 63; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHWSGHCL 9  
DB 1 AHWSGHCL 9

RESULT 2  
ADC42292  
ID ADC42292 standard; peptide; 9 AA.  
XX  
AC ADC42292;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Immunoglobulin light chain blocking peptide.  
XX  
KW gene therapy; immunoglobulin-free-light-chain receptor; Ig-LC receptor;  
KW signal transduction pathway activation; gamma-chain associated receptor;  
KW dermatitis; asthma; psoriasis; inflammatory bowel disease;  
KW rheumatoid arthritis; Sjogren lupus erythematosus;  
KW systemic lupus erythematosus; multiple sclerosis;  
KW Immunoglobulin light chain.  
XX  
OS Unidentified.  
XX  
PN WO2003074563-A2.  
XX  
PD 12-SEP-2003.  
XX  
PF 05-MAR-2003; 2003WO-NL000167.  
XX  
PR 06-MAR-2002; 2002EP-00075874.  
PR 06-MAR-2002; 2002US-0362040P.  
PR 14-JUN-2002; 2002EP-00077352.  
XX  
PA (FORN-) FORNIX BIOSCIENCES NV.  
XX  
PI Nijkamp EP, Redegeld FAM, Kraneveld AD, Van De Winkel JGJ;  
PI Vidarsson G;  
XX  
DR WPI; 2003-712878/67.  
XX  
PS New cell comprising an immunoglobulin-free-light-chain (Ig-LC) receptor  
PS that activates a signal transduction pathway in the cell, useful for  
PS selecting a compound capable of preventing binding of Ig-LC to the  
PS receptor.  
XX  
PS Example 3; Page 13; 69pp; English.  
XX

The invention comprises a cell containing an immunoglobulin-free-light-chain (Ig-LC) receptor that is capable of activating a signal transduction pathway in the cell upon binding of an Ig-LC to the receptor. The signal transduction is independent of the presence of a functional common gamma-chain associated receptor on the cell. The cell of the invention is useful for selecting a compound capable of preventing a binding of Ig-LC to the receptor. The cell is also useful for preparing a medicament for an animal suffering from or at risk of suffering from: dermatitis, asthma, psoriasis, inflammatory bowel disease, rheumatoid arthritis, Sjogren and systemic lupus erythematosus, and multiple sclerosis. The present amino acid sequence represents a peptide that binds to immunoglobulin light chains and therefore prevents the binding of the light chain to its receptor.

Query Match 100.0%; Score 63; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;

QY Sequence 9 AA;  
SQ

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHWSGHCL 9  
DB 1 AHWSGHCL 9

RESULT 3  
AAY21052  
ID AAY21052 standard; protein; 8 AA.  
XX  
AC AAY21052;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE Human glial fibrillary acidic protein GFAP mutant fragment 61.  
XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin 1; presenilin 2; semaphorin 3A; semaphorin 3B;  
KW glial fibrillary acidic protein; GFAP; p53; semaphorin 3A; semaphorin 3B;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9845322-A2.  
XX  
PD 15-OCT-1998.  
XX  
PF 02-APR-1998; 98WO-IB000705.  
XX  
PR 10-APR-1997; 97US-0043163P.  
XX  
PA (ROYA-) ROYAL NETHERLANDS ACADEMY OF ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
XX  
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;  
XX  
DR WPI; 1998-609901/51.  
DR N-PSDB; AAX75764.  
XX  
PS Diagnosing disease by detecting frameshift mutations in RNA or  
PS corresponding protein mutations - used to diagnose cancer and  
PS neurological diseases, particularly Alzheimer's disease, and also for  
PS treatment and prevention with specific ribozymes or wild-type RNA.  
XX  
PS Disclosure; Fig 13; 258pp; English.  
XX

This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins tau and big tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin 1, presenilin 2, semaphorin 3A, semaphorin 3B, protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin 3A, HMGP-C, NSP-A, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.



```

XX  Sequence 8 AA;
SQ
Query Match      57.1%; Score 36; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4 SGHCC 8
    |||||
Db  2 SGHCC 6

RESULT 4
AAB49950
ID  AAB49950 standard; peptide; 8 AA.
AC  AAB49950;
DT  07-MAR-2001 (first entry)
XX  Protein disulfide isomerase consensus N-terminus.
DE  Disulphide bond; allergy; protein disulfide isomerase variant; detergent;
XX  food additive; cosmetic.
XX  Mammalia.
XX  WO200070064-A1.
XX  23-NOV-2000.
XX  17-MAY-2000; 2000WO-DK000265.
XX  17-MAY-1999; 99DK-00000683.
XX  18-MAY-1999; 99DK-00000689.
XX  02-JUN-1999; 99US-0137068P.
XX  (NOVO ) NOVO NORDISK AS.
XX  Hjordt CM;
XX  WPI; 2001-070776/08.
XX  Protein disulfide isomerase variant having increased reducing properties
XX  and decreased redox potential than native proteins, used to reduce
XX  allergenicity of allergic proteins in feed, food or cosmetic products.
XX  Example 1; Page 33; 82pp; English.
XX  The present invention provides variants of the Aspergillus oryzae protein
XX  disulfide isomerase enzyme. These are capable of reducing disulphide
XX  bonds in proteins, which may be the cause of allergies in humans. The
XX  proteins can be used to reduce the allergenicity of foods, to treat
XX  scleroproteins, in detergents, in food additives and in cosmetics
XX  Sequence 9 AA;
XX  Query Match      55.6%; Score 35; DB 4; Length 9;
XX  Best Local Similarity 71.4%; Pred. No. 1.4e+06;
XX  Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AHWGHC 7
    |||||
Db  2 APWCGHC 8

RESULT 6
AAB49951
ID  AAB49951 standard; peptide; 6 AA.
AC  AAB49951;
XX  07-MAR-2001 (first entry)
XX  Protein disulfide isomerase consensus N-terminus.
XX  Disulphide bond; allergy; protein disulfide isomerase variant; detergent;
XX  food additive; cosmetic.
XX  Mammalia.
XX  WO200070064-A1.
XX  23-NOV-2000.
XX  17-MAY-2000; 2000WO-DK000265.
XX  17-MAY-1999; 99DK-00000683.
XX  18-MAY-1999; 99DK-00000689.
XX  02-JUN-1999; 99US-0137068P.
XX  (NOVO ) NOVO NORDISK AS.
XX  Hjordt CM;
XX  WPI; 2001-070776/08.
XX  Protein disulfide isomerase variant having increased reducing properties
XX  and decreased redox potential than native proteins, used to reduce
XX  allergenicity of allergic proteins in feed, food or cosmetic products.
XX  Example 1; Page 33; 82pp; English.
XX  The present invention provides variants of the Aspergillus oryzae protein
XX  disulfide isomerase enzyme. These are capable of reducing disulphide
XX  bonds in proteins, which may be the cause of allergies in humans. The
XX  proteins can be used to reduce the allergenicity of foods, to treat
XX  scleroproteins, in detergents, in food additives and in cosmetics
XX  Sequence 8 AA;
XX  Query Match      55.6%; Score 35; DB 4; Length 8;
XX  Best Local Similarity 71.4%; Pred. No. 1.4e+06;
XX  Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AHWGHC 7
    |||||
Db  1 APWCGHC 7

RESULT 5
AAB49952
ID  AAB49952 standard; peptide; 9 AA.
AC  AAB49952;
XX  07-MAR-2001 (first entry)

```

XX Hjort CM;  
 XX WPI; 2001-070776/08.  
 XX Protein disulfide isomerase variant having increased reducing properties  
 PT and decreased redox potential than native proteins, used to reduce  
 PT allergenicity of allergic proteins in feed, food or cosmetic products.  
 XX Example 1; Page 33; 82pp; English.  
 XX The present invention provides variants of the Aspergillus oryzae protein  
 CC disulfide isomerase enzyme. These are capable of reducing disulphide  
 CC bonds in proteins, which may be the cause of allergies in humans. The  
 CC proteins can be used to reduce the allergenicity of foods, to treat  
 CC scleroproteins, in detergents, in food additives and in cosmetics  
 XX Sequence 6 AA;  
 SQ

Query Match 52.4%; Score 33; DB 4; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WSGHC 7  
 DB 1 WCGHC 5

RESULT 7  
 ID ABP54937 standard; peptide; 6 AA.  
 AC ABP54937;  
 DT 08-JAN-2003 (first entry)  
 DE Active site peptide of protein disulfide isomerase.  
 KW Organoarsenical; arsenoxide; antiarthritic; antitumor; osteopoeitic;  
 KW antirheumatic; arthritis; therapy; protein disulfide isomerase; enzyme.  
 OS Homo sapiens.  
 XX WO200274305-A1.  
 XX 26-SEP-2002.  
 XX 19-MAR-2002; 2002WO-AU0000310.  
 XX 19-MAR-2001; 2001AU-00003798.  
 XX (UNIX) UNISEARCH LTD.  
 XX Hogg PJ, Donoghue N;  
 WPI; 2002-750519/81.  
 XX Use of an impermeable cell membrane compound for the treatment of  
 PT arthritis in vertebrates.  
 XX Example 2(b); Page 42; 91pp; English.  
 XX The present sequence is that of a hexapeptide comprising the active site  
 CC sequence of protein disulfide isomerase. The hexapeptide was used in an  
 CC example from the invention that examined the binding of 4-(N-(S-  
 CC glutathionylacetyl)amino)phenylarsenoxide (GSAO) to peptide and protein  
 CC dithiols. The results indicated that GSAO selectively binds proteins  
 CC containing closely spaced thiols. The invention provides a method for the  
 CC treatment and/or prophylaxis of arthritis using a compound of formula A-  
 CC (L-Y)p, where A is a cell-membrane impermeable pendant group, L is a  
 CC linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and p  
 CC is an integer from 1 to 10. The compound, e.g. GSAO, is useful for the  
 CC treatment of arthritic conditions such as calcific periarthritis,

CC enteropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid,  
 CC septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,  
 CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).  
 CC The compound blocks angiogenesis in the synovial tissue and leucocyte  
 CC ingress that triggers inflammation, with no signs or symptoms of toxicity  
 XX Sequence 6 AA;  
 SQ

Query Match 52.4%; Score 33; DB 5; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 WSGHC 7  
 DB 1 WCGHC 5

RESULT 8  
 AAW56315  
 ID AAW56315 standard; protein; 7 AA.  
 AC AAW56315;  
 DT 24-JUL-1998 (first entry)  
 DE Active centre of the disulphide bond exchange reaction catalysed by PDI.  
 KW Protein disulphide isomerase; PDI; methylotrophic yeast;  
 KW Candida boidinii strain S2; endoplasmic reticulum; stable conformation;  
 KW recombination; disulphide bond; secretory protein; gene therapy;  
 KW endoplasmic reticulum retention signal sequence; genetic engineering.  
 XX Candida boidinii.  
 XX EP828004-A2.  
 XX 11-MAR-1998.  
 XX 04-SEP-1997; 97EP-00306871.  
 XX 04-SEP-1996; 96JP-00234287.  
 XX (SUNR) SUNTORY LTD.  
 XX Sakai Y, Kato N, Shibano Y;  
 WPI; 1998-161102/15.  
 XX Methylotherophilic yeast protein disulphide isomerase - and corresponding  
 PT gene useful for increasing yields of secreted heterologous proteins in  
 PT Candida boidinii.  
 XX Example 1; Page 4; 30pp; English.  
 XX AAW56315-16 represent the active centre of the exchange reaction of  
 CC disulphide bonds, and are found in the protein disulphide isomerase (PDI)  
 CC derived from Candida boidinii. The sequences are related to AAW56314. PDI  
 CC is a major protein present in the lumen of the endoplasmic reticulum. PDI  
 CC is believed to be an enzyme which catalyses formation of stable  
 CC conformation by recombining disulphide bonds of secretory proteins. As  
 CC the protein must stay in the endoplasmic reticulum, it has a sequence  
 CC known as the endoplasmic reticulum retention signal sequence at the  
 CC carboxy terminus (AAW56317). The PDI protein is useful in gene therapy  
 CC and genetic engineering. The PDI gene may be coexpressed with a gene of  
 CC interest to ensure the production of a correctly folded biologically  
 CC active protein  
 XX Sequence 7 AA;  
 SQ

Query Match 52.4%; Score 33; DB 2; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 3 WSGHC 7
Db 2 WCGHC 6

RESULT 9
AA43470
ID AAY43470 standard; peptide; 7 AA.
XX AC AAY43470;
XX 27-AUG-2003 (revised)
DT 17-DEC-1999 (first entry)
XX DE Flavoprotein EpiD substrate determination peptide #31.
XX KW Staphylococcus epidermidis; epidermin; epiA; epiB; epiC; epiD; epiP; epiQ;
XX KW epiY; epiZ; oxidative carboxylation; flavoprotein.
XX OS Synthetic.
XX OS Staphylococcus epidermidis.
XX PN US5962253-A.
XX PD 05-OCT-1999.
XX PF 13-MAY-1996; 96US-00645193.
XX PR 13-MAY-1996; 96US-00645193.
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PI Kupke T, Kempter C, Jung G, Goetz F;
XX WPI; 1999-589714/50.
XX DR Oxidative decarboxylation of peptides by the flavoprotein EpiD.
XX PT Example 11; Col 37; 89pp; English.
XX PS The present invention describes the oxidative decarboxylation of a
CC peptide comprising combining the peptide which contains at its carboxy
CC terminus the amino acid sequence (I) with EpiD; X1-X2-X3-X4-X5-X6-C (I)
CC where X1, X2, X3 and X4 = any one of the 20 common amino acids; X5 = Tyr,
CC Val, Met, Phe, Ile, Leu or Trp; and X6 = Cys, Ala, Ser, Val or Thr
CC providing that the carboxy terminus of the peptide is not sequence (2)-
CC (5): SFNSVCC (2); SFNSVCC (3); SFNSVCC (4) and SFNSVCC (5). The method
CC can be used for the preparation of derivatives of known peptides and
CC hormones with a cysteine residue in the unmodified peptide replaced by
CC sulphide-bridged amino acids and serine and thiamine replaced by
CC corresponding dehydroamino acid residues. The formation of novel
CC compounds for experimental purposes or for the formation of known
CC compounds or their derivatives in new hosts e.g. biologically active
CC peptide derivatives containing dehydroamino acid residues and/or at least
CC one lanthionine bridge and/or methyl-lanthionine bridge such as
CC derivatives of human insulin, oxytocin, vasopressin, peptide antibiotics,
CC hormone inhibitors such as elastase inhibitor and fibrinolytically
CC active agents such as human tissue plasminogen activator can also be
CC achieved using this method. Derivatives modified by this method retain
CC the biological activity of the parent compound but have increased
CC stability and improved half-lives. AAY43470 to AAY43475, and AAY43496 to
CC AA225506, represent sequences used in the exemplification of the present
CC invention. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 7 AA;

Query Match 50.8%; Score 32; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WSGHC 8
Db 2 WNSVCC 7

RESULT 10
AAE19859
ID AAE19859 standard; peptide; 9 AA.
XX AC AAE19859;
XX 18-JUN-2002 (first entry)
DT TRIP zinc finger domain consensus.
XX DE Human; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
XX KW TRAF interacting protein; TRIP; cell activation; cell proliferation;
XX KW cell death; therapy; cytostatic; zinc finger domain.
XX OS Homo sapiens.
XX OS Mus sp.
XX PN US6346605-B1.
XX PD 12-FEB-2002.
XX PF 31-MAR-1998; 98US-00052089.
XX PR 01-APR-1997; 97US-0042293P.
XX PR 07-APR-1997; 97US-0042747P.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Lee SY, Choi Y;
XX WPI; 2002-225005/28.
XX DR New tumor necrosis factor receptor associated factor interacting protein,
XX PT useful for inhibiting NF-kappa B activation, and for modulating signals
XX PT responsible for cell activation, cell proliferation and cell death.
XX PS Example 2; Fig 2D; 37pp; English.
XX CC The present invention relates to a tumour necrosis factor (TNF) receptor
CC associated factor (TRAF) interacting protein (TRIP), which is a regulator
CC capable of binding to TRAF2. TRIP is useful for inhibiting NF-kappa B
CC activation and for modulating signals responsible for cell activation,
CC cell proliferation and cell death. Thus, TRIP is useful for treating
CC diseases associated with altered cell proliferation and cell death. The
CC present sequence is zinc finger domain consensus sequence of human and
CC mouse TRIP
XX SQ Sequence 9 AA;

Query Match 50.8%; Score 32; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GHCC 8
Db 4 GHCC 7

RESULT 11
AA23018
ID AAM23018 standard; peptide; 9 AA.
XX AC AAM23018;
XX 22-OCT-2001 (first entry)
DT HIV peptide SEQ ID NO 903.
XX KW Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX KW human immunodeficiency virus; vaccine.
XX SQ
```

OS Human immunodeficiency virus.  
 OS Synthetic.  
 PN WO200155177-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 29-JAN-2001; 2001WO-DK000059.  
 XX  
 XX 28-JAN-2000; 2000EP-00610017.  
 PR 31-JAN-2000; 2000US-0179333P.  
 XX  
 XX (STAT-) SPATENS SERUM INST.  
 XX

PI Ponsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
 XX WPI; 2001-476184/51.  
 XX  
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-  
 XX HIV vaccines.  
 PT  
 XX

PS Example 4; Page 70; 383pp; English.  
 XX

XX The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents  
 CC

SQ Sequence 9 AA;  
 XX

Query Match 49.2%; Score 31; DB 4; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WSGHCCCL 9  
 | : | | |  
 DB 3 WATIACL 9

RESULT 12  
 AAU23853  
 ID AAU23853 standard; peptide; 9 AA.  
 XX  
 XX AAU23853;  
 AC

DT 17-DEC-2001 (first entry)  
 XX

DE Human MHC class I molecule HLA-A1 binding 103P2D6 peptide #38.  
 XX

XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX

OS Homo sapiens.  
 XX

PN WO200162925-A2.  
 XX

PD 30-AUG-2001.  
 XX

PF 26-FEB-2001; 2001WO-US005996.  
 XX

XX 24-FEB-2000; 2000US-0184558P.  
 PR

PR 13-JUL-2000; 2000US-0218856P.  
 XX

XX (UROC-) UROGENESYS INC.  
 PA

PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-Eid PM, Faris M, Jakobovits A;  
 XX

DR WPI; 2001-557705/62.  
 XX

PT New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 XX

PS Example 15; Page 81; 132pp; English.  
 XX

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells  
 XX

SQ Sequence 9 AA;  
 XX

Query Match 49.2%; Score 31; DB 4; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WSGHCCCL 9  
 | : | | |  
 DB 1 WSGRCGL 7

RESULT 13  
 AAU24423  
 ID AAU24423 standard; peptide; 9 AA.  
 XX  
 XX AAU24423;  
 AC

DT 17-DEC-2001 (first entry)  
 XX

DE Human MHC molecule HLA-B35 binding 103P2D6 peptide #8.  
 XX

XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX

OS Homo sapiens.  
 XX

PN WO200162925-A2.  
 XX

PD 30-AUG-2001.  
 XX

PF 26-FEB-2001; 2001WO-US005996.  
 XX

XX 24-FEB-2000; 2000US-0184558P.  
 PR

PR 13-JUL-2000; 2000US-0218856P.  
 XX

XX (UROC-) UROGENESYS INC.  
 PA

PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-Eid PM, Faris M, Jakobovits A;  
 XX

XX WPI; 2001-557705/62.  
 DR

XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 PT

PS Example 15; Page 97; 132pp; English.  
 XX

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and

CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells  
 XX  
 SQ Sequence 9 AA;

Query Match 49.2%; Score 31; DB 4; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WSGHCCL 9  
 |||||  
 Db 1 WSGRCGL 7

RESULT 14  
 AAU24453  
 ID AAU24453 standard; peptide; 9 AA.

AC AAU24453;

XX 17-DEC-2001 (first entry)

XX Human MHC molecule HLA-B35 binding 103P2D6 peptide #38.

XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.

XX Homo sapiens.

OS WO200162925-A2.

PN 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US0005996.

XX 24-FEB-2000; 2000US-0184558P.

PR 13-JUL-2000; 2000US-0218856P.

XX (UROG-) UROGENESYS INC.

XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Chailita-Eid PM, Faris M, Jakobovits A;

XX WPI; 2001-557705/62.

XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.

XX Example 15; Page 98; 132pp; English.

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells  
 XX  
 SQ Sequence 9 AA;

Query Match 47.6%; Score 30; DB 4; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WSGHC 7  
 |||||  
 Db 5 WSGRC 9

RESULT 15  
 ABB05276  
 ID ABB05276 standard; peptide; 9 AA.

XX ABB05276;

XX 29-AUG-2003 (revised)

DT 04-APR-2002 (first entry)

XX Vascular endothelial growth factor binding peptide BP 86 SEQ ID NO:108.

XX Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain;  
 KW bacteriophage; phage library; vascular endothelial growth factor;  
 KW collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.

XX Unidentified bacteriophage.

OS Unidentified.

XX WO200179479-A2.

XX 25-OCT-2001.

XX 11-APR-2001; 2001WO-US011811.

PR 14-APR-2000; 2000US-0197259P.

XX (GENV) GENENCOR INT INC.

XX Estell DA, Murray CJ, Tijerina P, Chen Y;

XX WPI; 2002-139323/18.

XX Screening ligand library comprises allowing binding of ligand with anti-  
 PT target, contacting unbound ligands with selected target to form target-  
 PT bound ligand complex and identifying target bound ligands on the complex.

XX Claim 23; Page 28; 51pp; English.

XX The present invention describes a method for screening a ligand library  
 CC (LL). The method comprises: (a) contacting the LL with an anti-target  
 CC (AT) to allow the ligands to bind to the AT; (b) separating unbound  
 CC ligands; (c) contacting the unbound ligands with a selected target (T) to  
 CC allow binding of unbound ligands to (T) to form a (T)-bound ligand  
 CC complex (C); (d) separating (C) from ligands which do not bind (T); and  
 CC (e) identifying (T)-bound ligands on (C). The method can be used for  
 CC screening a ligand library, e.g., a library of peptides, polypeptides,  
 CC non-polypeptides or oligonucleotides. A ligand (I) identified by the  
 CC method can be used in a cleaning, therapeutic or personal care  
 CC application. The method is preferably useful for identifying peptides  
 CC useful in cleaning compositions, which involves contacting peptide  
 CC library with AT such as fabric, ceramic, glass, stainless steel or  
 CC plastic; separating unbound AT peptides; contacting unbound AT peptides  
 CC with a target which is a stain such as porphyrin derived stain; tannin  
 CC derived stain, carotenoid pigment derived stain, anthocyanin pigment  
 CC derived stain, soil-based derived stain, oil-based derived stain, and

CC human body stain, to allow unbound peptide to bind with the stain to form  
CC stain-bound peptide complex and identifying the stain-bound peptide on  
CC the stain-bound peptide complex. A selective targeting method for  
CC screening a library of ligands that bind to a target may be used to  
CC identify ligands that bind to a target under harsh conditions. The  
CC selective targeting method may be used to screen and identify a ligand  
CC useful for therapeutic intervention, e.g., a library of ligands may be  
CC screened to identify a tumour-bound ligand. The selective targeting  
CC method may be used to identify cell type specific surface molecules.  
CC Preferred anti-targets include one or more different cell types, cells in  
CC different states, or cells that do not display the surface molecule.  
CC ABB05232 to ABB05346 represent phage-peptides ligands which are used in  
CC the exemplification of the present invention. (Updated on 29-AUG-2003 to  
CC standardise OS field)

XX  
SQ Sequence 9 AA;

Query Match 47.6%; Score 30; DB 5; Length 9;  
Best Local Similarity 50.0%; Pred. NO. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RHWSGHCC 8  
| | | |  
Db 2 APWNSHC 9

Search completed: June 1, 2004, 10:26:56  
Job time : 56 secs

GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: June 1, 2004, 10:28:21 ; Search time 42 Seconds  
(without alignments)  
59,833 Million cell updates/sec

Title: US-09-756-899A-1

Sequence: 1 AHWSGHCHCL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 110747

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PTCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	63	100.0	9	9	US-09-756-899A-1
2	36	57.1	5	12	US-10-436-549-494
3	31	49.2	9	10	US-09-793-451-52
4	31	49.2	9	10	US-09-793-451-622
5	31	49.2	9	12	US-10-182-252A-903
6	31	49.2	9	14	US-10-283-722-52
7	31	49.2	9	14	US-10-283-722-622
8	31	49.2	9	15	US-10-283-903-52
9	31	49.2	9	15	US-10-283-903-622
10	30	47.6	5	12	US-10-436-549-497
11	30	47.6	9	9	US-09-832-723-108
12	30	47.6	9	10	US-09-793-451-652
13	30	47.6	9	14	US-10-303-331-108
14	30	47.6	9	14	US-10-283-722-652
15	30	47.6	9	15	US-10-283-903-652

Sequence 46, Appl  
Sequence 289, App  
Sequence 906, App  
Sequence 1180, Ap  
Sequence 1182, Ap  
Sequence 118, App  
Sequence 117, App  
Sequence 87, Appl  
Sequence 107, App  
Sequence 104, App  
Sequence 70, Appl  
Sequence 23, Appl  
Sequence 109, App  
Sequence 6, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 116, App  
Sequence 217, App  
Sequence 226, App  
Sequence 306, App  
Sequence 331, App  
Sequence 413, App  
Sequence 502, App  
Sequence 531, App  
Sequence 610, App  
Sequence 63, Appl  
Sequence 89, Appl  
Sequence 151, App

US-08-821-739A-46  
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US-10-182-252A-906  
US-10-182-252A-1180  
US-10-182-252A-1182  
US-10-254-446A-118  
US-10-360-101-117  
US-09-911-838-87  
US-10-096-986-107  
US-10-396-122-104  
US-10-430-685-70  
US-10-197-927-23  
US-09-832-723-109  
US-10-216-810A-6  
US-10-303-331-109  
US-10-362-768A-2  
US-09-938-114-6  
US-09-942-052-116  
US-09-942-052-217  
US-09-942-052-226  
US-09-942-052-306  
US-09-942-052-331  
US-09-942-052-413  
US-09-942-052-502  
US-09-942-052-531  
US-09-942-052-610  
US-10-357-173-63  
US-10-455-720-63  
US-10-360-101-89  
US-10-254-446A-151

ALIGNMENTS

RESULT 1

US-09-756-899A-1  
; Sequence 1, Application US/09756899A  
; Patent No. US20020045186A1  
; GENERAL INFORMATION:  
; APPLICANT: Redgeld, Francisus  
; APPLICANT: Kraneveld, Aletta  
; APPLICANT: Nijkamp, Francisus  
; TITLE OF INVENTION: INHIBITION OF PROTEIN BINDING TO MAST CELLS  
; FILE REFERENCE: 2183-4692  
; CURRENT APPLICATION NUMBER: US/09/756,899A  
; CURRENT FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: PCT/NL99/00430  
; PRIOR FILING DATE: 1997-07-07  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: peptide  
US-09-756-899A-1

Query Match 100.0%; Score 63; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No 1e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHWSGHCHCL 9

DB 1 AHWSGHCHCL 9

RESULT 2

US-10-436-549-494  
; Sequence 494, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:

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; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Xun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng J.
; APPLICANT: Benkovic, Stephen J.
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: ENGE-P01-001
; CURRENT APPLICATION NUMBER: US/10/436,549
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/433,319
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 494
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-10-436-549-494

Query Match 57.1%; Score 36; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GHCCCL 9
Db 1 GHCCCL 5

RESULT 3
US-09-793-451-52
; Sequence 52, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6; TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.20SU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-622

Query Match 49.2%; Score 31; DB 10; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WSGHCCL 9
Db 1 WSGRCGL 7

RESULT 5
US-10-182-252A-903
; Sequence 903, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
```

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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-52

Query Match 49.2%; Score 31; DB 10; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WSGHCCL 9
Db 1 WSGRCGL 7

RESULT 4
US-09-793-451-622
; Sequence 622, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 103P2D6; TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.20SU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-622

Query Match 49.2%; Score 31; DB 10; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WSGHCCL 9
Db 1 WSGRCGL 7

RESULT 5
US-10-182-252A-903
; Sequence 903, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
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; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 903  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-903

Query Match 49.2%; Score 31; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1e+06; 2; Indels  
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 3 WSGHCCL 9  
|: |||  
DB 3 WATHACL 9

RESULT 6  
US-10-283-722-52  
; Sequence 52, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-52

Query Match 49.2%; Score 31; DB 14; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1e+06; 2; Indels  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 3 WSGHCCL 9  
|: |||  
DB 1 WSGRCGL 7

RESULT 7  
US-10-283-722-622  
; Sequence 622, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Mary Faris

; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 622  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-622

Query Match 49.2%; Score 31; DB 14; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1e+06; 2; Indels  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 3 WSGHCCL 9  
|: |||  
DB 1 WSGRCGL 7

RESULT 8  
US-10-283-903-52  
; Sequence 52, Application US/10283903  
; Publication No. US20030219766A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,903  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-903-52

Query Match 49.2%; Score 31; DB 15; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1e+06; 2; Indels  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 3 WSGHCCL 9  
|: |||  
DB 1 WSGRCGL 7

RESULT 9  
US-10-283-903-622  
; Sequence 622, Application US/10283903

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; Publication No. US20030219766A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT FILING DATE: 2003-02-03
; CURRENT APPLICATION NUMBER: US/10/283,903
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-283-903-622

Query Match      49.2%; Score 31; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 WSGHCC 9
   |||||
Db 1 WSGRGL 7

RESULT 10
US-10-436-549-497
; Sequence 497, Application US/10436549
; Publication No. US20040038307A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Xun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng
; APPLICANT: Benkovic, Stephen J.
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
; FILE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: ENGE-P01-001
; CURRENT APPLICATION NUMBER: US/10/436,549
; CURRENT FILING DATE: 2003-05-12
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/433,319
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
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; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 497
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
; US-10-436-549-497

Query Match      47.6%; Score 30; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HCCL 9
   |||||
Db 1 HCCL 4

RESULT 11
US-09-832-723-108
; Sequence 108, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
; US-09-832-723-108

Query Match      47.6%; Score 30; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AHWGHC 8
   ||:|
Db 2 APWNSHC 9

RESULT 12
US-09-793-451-652
; Sequence 652, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
```

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; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-652

Query Match      47.6%; Score 30; DB 10; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 WSGHC 7
      |||||
Db      5 WSGRC 9

RESULT 13
US-10-303-331-108
; Sequence 108, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
US-10-303-331-108

Query Match      47.6%; Score 30; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AFWSHGCC 8
      |||||
Db      2 APWNSHC 9

RESULT 14
US-10-283-722-652
; Sequence 652, Application US/10283722
; Publication No. US2003019407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-652

Query Match      47.6%; Score 30; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 WSGHC 7
      |||||
Db      5 WSGRC 9

Search completed: June 1, 2004, 10:33:57
Job time : 43 secs
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